

INTERIM REPORT

“SHARE WITH WILDLIFE” GRANT: Genetic and Species Diversity in *Popenaias* (Bivalvia: Unionoida: Unionidae: Lampsilini) populations from New Mexico and Texas.

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Statement Of The Objectives, Goals, And Tasks

Program Summary: Unionoid bivalves (freshwater mussels) exhibit a relatively high degree of inter-individual variation in shell morphology such that species diversity and species limits are, typically, inadequately understood for this group of organisms.

The proposed study will generate estimates of genetic and species diversity for *Popenaias* bivalve populations in New Mexico and Texas, and include these data in a larger systematic analysis of North American lampsiline freshwater mussels. Estimates of genetic differentiation will be based on DNA sequence data obtained from two independent genetic loci, the female (F)- and male (M)-transmitted mitochondrial DNA genomes. These relatively fast evolving and independent loci will allow for multiple evaluations of genetic and species diversity.

These evaluations will provide resource management professionals with the information required to make informed conservation decisions regarding the Texas hornshell (*Popenaias popeii*), a state endangered mussel (NMDGF 2006a) and a federal candidate for listing (priority 2) under the Endangered Species Act (Federal Register 2001). Genetic study of this species is called for under the state recovery plan (NMDGF 2007: 46) and the “*Comprehensive Wildlife Conservation Strategy for New Mexico*” (NMDGF 2006b: 335).

Project Objectives:

- 1) Analyze tissues from individuals of the Texas hornshell mussel (*Popenaias popeii*) from New Mexico and Texas. The tissues required for the proposed genetic comparisons are already housed in Hoeh’s lab at KSU. A maximum of 100 *P. popeii* tissue samples will be analyzed.
- 2) Extract DNA from mantle (and testes [when available]) tissue samples to access F and M mitochondrial DNA genomes from the sampled individuals.
- 3) Perform polymerase chain reaction (PCR) amplifications and automated DNA sequencing of F and M mtDNA fragments containing cytochrome *c* oxidase subunit I (*COI*) gene sequences.

- 4) Quantify the distribution of F and M *COI* sequence variation within and among populations of the Texas hornshell mussel (*Popenaias popeii*).
- 5) Use species-specific DNA sequences, representing geographically extralimital populations of other lampsiline bivalves (for comparative purposes), to estimate the contextual genetic relationships among *P. popeii* individuals and populations using Bayesian inference, maximum likelihood and maximum parsimony tree-building techniques.
- 6) Use the phylogenetic species concept in conjunction with levels of among- and within-population differentiation in F and M *COI* sequences to evaluate the genetic and species diversity in the Texas hornshell mussel (*Popenaias popeii*).
- 7) Submit a detailed final report to the NMDGF containing the findings of the research project.

Results to date:

- 1) *Popenaias popeii* (from NM) *Fcox1* (EF033257) and *Mcox1* (EF033294) mtDNA sequences were generated in my lab and are now available on GenBank.
- 2) The foundational research necessary for estimating the contextual genetic relationships among *P. popeii* populations and those of lampsiline bivalve species, which made use of both *Fcox1* and *Mcox1* sequences, has been published in the journal *Malacologia* (2008; Vol. 50: 303-318).
- 3) Tissues from 11 *P. popeii* specimens from NM (collected by Brian Lang) have been processed in my lab and *Fcox1* sequences have been obtained.
- 4) Preliminary genetic analysis of these 11 NM *P. popeii* *Fcox1* sequences indicated intra-population sequence variation. Thus, it would not be surprising to observe significant mtDNA sequence divergence between NM and TX populations of *P. popeii*.
- 5) Tissues from 13 *P. popeii* specimens from TX (collected by Tom Miller) have been processed in my lab and *Fcox1* sequences have been obtained.
- 6) Tissues from an additional eight *P. popeii* specimens from TX (also collected by Tom Miller) have been extracted for total DNA and PCR amplicons from the *Fcox1* gene have been obtained.

In summary, I feel that significant progress has been made on this project despite the relatively short time period that the contract has been in effect and that this bodes well for the successful and timely completion of the project.